SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> Novel G protein-coupled receptors

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<151> 1998-10-09

<150> JP 1998-347546

<151> 1998-12-07

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Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe
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Glu Ile Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile
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Cys Thr Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile
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Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly
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Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly
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Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Leu

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230 235 240

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Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro Leu Asp Gly
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295 300 305

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Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile
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Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr
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Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu
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Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser
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Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr
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Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu
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Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser
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Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser

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Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro

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Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys

115 120 125

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Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp

165 170 175

Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp

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Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val

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225 230 235 240

Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys

245 250 255

Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala

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Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile

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Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala

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Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu

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Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr

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Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg

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Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His

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Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro

165 170 175

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu

180 185 190

Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val

195 200 205

Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala

210 215 220

Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg

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Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr

245 250 255

Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro

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ctgagcgcct tgcttgtggc tggagcctgg atggcaggat ccatccatgg ggctctccag 480

gccatcctaa ccttccgcct gccctactgt gggcccaatc aggtggatta cttcttctgt 540

gacatccctg cagtgttgag actggcctgt gctgacacaa cagtcaacga gctggtgacg 600

tttgtagaca ttggggtggt ggttgccagt tgcttctccc tgatcctcct ctcctacata 660

cagatcattc aggccatcct gagaatccac acagctgatg ggcggcgccg ggctttttca 720

acttgtggag cccatgtaac cgtggtcacc gtgtactatg tgccctgtgc cttcatctac 780

ctgaggcctg aaaccaacag ccccctggat ggggcagctg ccctagtccc cacggccatc 840

actcctttcc tcaacccccc tatctacact ctgcggaacc aagaggtgaa gctggccctg 900

aaaagaatgc tcagaagccc aagaactccg agtgaggttt ga 942

<210> 23

<211> 933

<212> DNA

<213> Homo sapiens

<400> 23

atgggaaaga ccaaaaacac atcgctggat gccgtggtga cagatttcat tcttctgggt 60

ttgtctcacc ccccaaatct aagaagcctc ctcttcctgg tcttcttcat catttacatc 120

ctcactcagc tggggaacct gctcattctg ctcaccatgt gggctgaccc gaagctctgt 180

gctcgcccca tgtacattct tctgggagtg ctctcattcc tggacatgtg gctctcctca 240

gtcaccgttc ctcggcttat tttggatttt actccttcca tcaaggctat cccgtttggt 300

ggctgtgtgg ctcaactgta tttctttcac ttcctgggca gcacccagtg cttcctctac 360

accttgatgg cctatgacag gtacctagca atatgtcagc ccctgcacta cccagtgctc 420

atgaatggga ggttatgcac agtccttgtg gctggagctt gggtcgccgg ctccatgcat 480

gggtctatcc aggccacctt gaccttccgc ctgccctact gtgggcccaa tcaggtggat 540

tactttatct gtgacatccg cgcagtattg agactggcct gtgctgacac aactgtcaat 600

gagcttgtga cctttgtgga cgtcagggta gtggccgcca gttgcttcat gttaattctg 660

ctctcctatg ccaacatagt ccatgccatc ctgaagatac gcaccgctga tgggaggcgc 720

cgggccttct ccacctgtgg ctcccaccta atcgtggtca cagtctacta tgtcccctgt 780

attttcatct accttagggc tggctccaaa gacccccctgg atggggcagc ggctgtgttt 840

tacactgttg tcactccatt actgaacccc ctcatctata cactgaggaa ccaggaagtg 900

aagtctgccc tgaagaggat aacagcaggt tga 933

<210> 24

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)..(892)

<400> 24

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1 5 10

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc 100
Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe
15 20 25

ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc 148
Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly
30 35 40

atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac 196
Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr
45 50 55 60

tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc 244
Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val
65 70 75

att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc 292
Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile
80 85 90

ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg 340
Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val
95 100 105

gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt 388
Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val

110 115 120

gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc 436
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val
125 130 135 140

tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc 484
Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala
145 150 155

ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac 532
Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His
160 165 170

att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc 580
Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser
175 180 185

tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg 628
Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly
190 195 200

ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc 676
Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe
205 210 215 220

atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa 724
Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys
225 230 235

gct ttt gga aca tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt 772
Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe
240 245 250

ggg tcc att acc ttc atg tat ttc aag ccc cct tca agt aac tcc ctg 820
Gly Ser Ile Thr Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu
255 260 265

gac cag gag aag gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg 868
Asp Gln Glu Lys Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met
270 275 280

ctg aac cct tta ata tac agt ctg taatcacagc actttggaag gctgaggcag 922
Leu Asn Pro Leu Ile Tyr Ser Leu
285 290

ggttgcttga gtccagtttg agaccatcct ggggaacata gtgcgatctt gtttctttcc 982

actgcctaaa aacttcaatg ctcaatttta cttgcaattt cctcttcctg acatggagaa 1042

tgttggcttg gaatgttc 1060

<210> 25

<211> 1069

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(956)

<400> 25

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Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu
1 5 10

ttt att ctt gct gga tta aca gat cgt cca gag ttc tgg caa ccc ttc 98
Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe
15 20 25

ttt ttc ctg ttc cta gtg atc tac att gtc acc atg gta ggc aac ctt 146
Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu
30 35 40

ggc ttg atc act ctt ttc ggt cta aat tct cac ctc cac aca cca atg 194
Gly Leu Ile Thr Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met
45 50 55

tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct 242
Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser
60 65 70 75

gtt ttc act ccc aaa atg cta atg aac ttt gtg tca aaa aag aat att 290
Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile
80 85 90

atc tcc aat gtt ggg tgc atg act cgg ctg ttt ttc ttt ctc ttt ttc 338
Ile Ser Asn Val Gly Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe
95 100 105

gtc atc tct gaa tgt tac atg ttg acc tca atg gca tat gat cgc tat 386
Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr
110 115 120

gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag 434
Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln
125 130 135

gtc tgt tct atg ctc act ttt gct gct tac ata atg gga ttg gct gga 482
Val Cys Ser Met Leu Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly
140 145 150 155

gcc acg gcc cac acc ggg tgc atg ttt aga ctc acc ttc tgc agt gct 530

Ala Thr Ala His Thr Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala
160 165 170

aat atc att aac cat tac ttg tgt gac ata ctc ccc ctc ctc cag ctt 578
Asn Ile Ile Asn His Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu
175 180 185

tcc tgc acc agc acc tat gtc aac gag gtg gtt gtt ctc att gtt gtg 626
Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val Val Leu Ile Val Val
190 195 200

ggt act aat atc acg gta ccc agt tgt acc atc ctc att tct tat gtt 674
Gly Thr Asn Ile Thr Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val
205 210 215

ttc att gtc act agc att ctt cat atc aaa tcc act caa gga aga tca 722
Phe Ile Val Thr Ser Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser
220 225 230 235

aaa gcc ttc agt act tgt agc tct cat gtc att gct ctg tct ctg ttt 770
Lys Ala Phe Ser Thr Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe
240 245 250

ttt ggg tca gcg gca ttc atg tat att aaa tat tct tct gga tct atg 818
Phe Gly Ser Ala Ala Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met
255 260 265

gag cag gga aaa gtt ttt tct gtt ttc tac act aat gtg gtg ccc atg 866
Glu Gln Gly Lys Val Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met
270 275 280

ctc aat ccc ctc atc tac agt ttg agg aac aag gat gtc aaa gtt gca 914
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala
285 290 295

ctg agg aaa gct ctg att aaa att cag agg aga aat ata ttc 956
Leu Arg Lys Ala Leu Ile Lys Ile Gln Arg Arg Asn Ile Phe
300 305 310

taattagaag cagtaatgat gtaaaacaat tgaaggactt caaattttta ttagtgtttt 1016

tcatgaagag attttgttgt ttctacagat ggtgttatgt gtgatttaat aaa 1069

<210> 26
<211> 1069
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18)..(956)

<400> 26

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Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu
1 5 10

ttt att ctt gct gga tta aca gat cgt cca gag ttc cgg caa ccc ctc 98
Phe Ile Leu Ala Gly Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu
15 20 25

ttt ttc ctg ttt cta gtg atc tac att gtc acc atg gta ggc aac ctt 146
Phe Phe Leu Phe Leu Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu
30 35 40

ggc ttg atc att ctt ttc ggt cta aat tct cac ctc cac aca cca atg 194
Gly Leu Ile Ile Leu Phe Gly Leu Asn Ser His Leu His Thr Pro Met
45 50 55

tac tat ttc ctc ttc aat ctc tcc ttc att gat ctc tgt tac tcc tct 242
Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser
60 65 70 75

gtt ttc act ccc aaa atg cta atg aac ttt gta tca aaa aag aat att 290
Val Phe Thr Pro Lys Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile
80 85 90

atc tcc tat gtt ggg tgc atg act cag ctg ttt ttc ttt ctc ttt ttt 338
Ile Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe
95 100 105

gtc atc tct gaa tgc tac ata ttg acc tca atg gca tat gat cgc tat 386
Val Ile Ser Glu Cys Tyr Ile Leu Thr Ser Met Ala Tyr Asp Arg Tyr
110 115 120

gtg gcc atc tgt aat cca ttg ctg tat aag gtc acc atg tcc cat cag 434
Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln
125 130 135

gtc tgt tct atg ctc act ttt gct gct tac ata atg gga ttg gct gga 482
Val Cys Ser Met Leu Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly
140 145 150 155

gcc acg gcc cac acc ggg tgc atg ctt aga ctc acc ttc tgc agt gct 530
Ala Thr Ala His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala
160 165 170

aat atc atc aac cat tac ttg tgt gac ata ctc ccc ctc ctc cag ctt 578
Asn Ile Ile Asn His Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu
175 180 185

tcc tgc acc agc acc tat gtc aac gag gtg gtt gtt ctc att gtt gtg 626
Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val Val Leu Ile Val Val

190 195 200

ggt att aat atc atg gta ccc agt tgt acc atc ctc att tct tat gtt 674
Gly Ile Asn Ile Met Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val
205 210 215

ttc att gtc act agc att ctt cat atc aaa tcc act caa gga aga tca 722
Phe Ile Val Thr Ser Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser
220 225 230 235

aaa gcc ttc agt act tgt agc tct cat gtc att gct ctg tct ctg ttt 770
Lys Ala Phe Ser Thr Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe
240 245 250

ttt ggg tca gcg gca ttc atg tat att aaa tat tct tct gga tct atg 818
Phe Gly Ser Ala Ala Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met
255 260 265

gag cag gga aaa gtt tct tct gtt ttc tac act aat gtg gtg ccc atg 866
Glu Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met
270 275 280

ctc aat cct ctc atc tac agt ttg agg aac aag gat gtc aaa gtt gca 914
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala
285 290 295

ctg agg aaa gct ctg att aaa att cag aga aga aat ata ttc 956
Leu Arg Lys Ala Leu Ile Lys Ile Gln Arg Arg Asn Ile Phe
300 305 310

taattagaag cagtaataat gtaaaacgat tgaagaactt taaattttta ttagtgtgtt 1016

ccatgaagag attttgttgt ttctacagat ggtgttatgt gtgatttaat aaa 1069

<210> 27
<211> 976
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (19)..(945)

<400> 27
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Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu
1 5 10

ttt atc ctt gtg gga tta tca gaa cag cca gag ctc cag ctc cct ctt 99
Phe Ile Leu Val Gly Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu
15 20 25

ttc ctt cta ttc tta ggg atc tat gtg ttc act gtg gtg ggc aac ttg 147
Phe Leu Leu Phe Leu Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu
30 35 40

ggc ttg atc acc tta att ggg ata aat cct agc ctt cac acc ccc atg 195
Gly Leu Ile Thr Leu Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met
45 50 55

tac ttt ttc ctc ttc aac ttg tcc ttt ata gat ctc tgt tat tcc tgt 243
Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys
60 65 70 75

gtg ttt acc ccc aaa atg ctg aat gac ttt gtt tca gaa agt atc atc 291
Val Phe Thr Pro Lys Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile
80 85 90

tct tat gtg gga tgt atg act cag cta ttt ttc ttc tgt ttc ttt gtc 339
Ser Tyr Val Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val
95 100 105

aat tct gag tgc tat gtg ttg gta tca atg gcc tat gat cgc tat gtg 387
Asn Ser Glu Cys Tyr Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val
110 115 120

gcc atc tgc aac ccc ctg ctc tac atg gtc acc atg tcc cca agg gtc 435

Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val
125 130 135

tgc ttt ctg ctg atg ttt ggt tcc tat gtg gta ggg ttt gct ggg gcc 483
Cys Phe Leu Leu Met Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala
140 145 150 155

atg gcc cac act gga agc atg ctg cga ctg acc ttc tgt gat tcc aac 531
Met Ala His Thr Gly Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn
160 165 170

gtc att gac cat tat ctg tgt gac gtt ctc ccc ctc ttg cag ctc tcc 579
Val Ile Asp His Tyr Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser
175 180 185

tgc acc agc acc cat gtc agt gag ctg gta ttt ttc att gtt gtt gga 627
Cys Thr Ser Thr His Val Ser Glu Leu Val Phe Phe Ile Val Val Gly
190 195 200

gta atc acc atg cta tcc agc ata agc atc gtc atc tct tac gct ttg 675
Val Ile Thr Met Leu Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu
205 210 215

ata ctc tcc aac atc ctc tgt att cct tct gca gag ggc aga tcc aaa 723
Ile Leu Ser Asn Ile Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys
220 225 230 235

gcc ttt agc aca tgg ggc tcc cac ata att gct gtt gct ctg ttt ttt 771
Ala Phe Ser Thr Trp Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe
240 245 250

ggg tca ggg aca ttc acc tac tta aca aca tct ttt cct ggc tct atg 819
Gly Ser Gly Thr Phe Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met
255 260 265

aac cat ggc aga ttt gcc tca gtc ttt tac acc aat gtg gtt ccc atg 867
Asn His Gly Arg Phe Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met
270 275 280

ctt aac cct tcg atc tac agt ttg agg aat aag gat gat aaa ctt gcc 915
Leu Asn Pro Ser Ile Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala
285 290 295

ctg ggc aaa acc ctg aag aga gtg ctc ttc taatgggtct cttcatatca 965
Leu Gly Lys Thr Leu Lys Arg Val Leu Phe
300 305

ctggcaaccg a 976

<210> 28

<211> 292

<212> PRT

<213> Homo sapiens

<400> 28

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
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Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20 25 30

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
35 40 45

Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50 55 60

Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
65 70 75 80

Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
85 90 95

Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
100 105 110

Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser

115 120 125

Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
130 135 140

Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
145 150 155 160

Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
165 170 175

Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
180 185 190

His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
195 200 205

Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
210 215 220

Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225 230 235 240

Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
245 250 255

Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
260 265 270

Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
275 280 285

Ile Tyr Ser Leu
290

<210> 29
<211> 313
<212> PRT
<213> Homo sapiens

<400> 29
Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
1 5 10 15

Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu
20 25 30

Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
35 40 45

Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe

50 55 60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65 70 75 80

Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
85 90 95

Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
100 105 110

Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115 120 125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
130 135 140

Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145 150 155 160

Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
165 170 175

Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
180 185 190

Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
195 200 205

Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210 215 220

Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225 230 235 240

Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245 250 255

Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
260 265 270

Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
275 280 285

Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
290 295 300

Ile Lys Ile Gln Arg Arg Asn Ile Phe
305 310

<210> 30

<211> 313

<212> PRT

<213> Homo sapiens

<400> 30

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
1 5 10 15

Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
20 25 30

Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Ile Leu
35 40 45

Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
50 55 60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65 70 75 80

Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Tyr Val Gly
85 90 95

Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
100 105 110

Tyr Ile Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115 120 125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
130 135 140

Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145 150 155 160

Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
165 170 175

Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
180 185 190

Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
195 200 205

Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210 215 220

Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225 230 235 240

Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245 250 255

Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
260 265 270

Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
275 280 285

Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
290 295 300

Ile Lys Ile Gln Arg Arg Asn Ile Phe
305 310

<210> 31
<211> 309
<212> PRT
<213> Homo sapiens

<400> 31
Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
1 5 10 15

Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20 25 30

Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
35 40 45

Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
50 55 60

Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
65 70 75 80

Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
85 90 95

Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
100 105 110

Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
115 120 125

Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met
130 135 140

Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly
145 150 155 160

Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
165 170 175

Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
180 185 190

Val Ser Glu Leu Val Phe Phe Ile Val Val Gly Val Ile Thr Met Leu
195 200 205

Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile
210 215 220

Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Trp
225 230 235 240

Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe Gly Ser Gly Thr Phe
245 250 255

Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Asn His Gly Arg Phe
260 265 270

Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Ser Ile
275 280 285

Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala Leu Gly Lys Thr Leu
290 295 300

Lys Arg Val Leu Phe

305

<210> 32

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 32

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Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe
1 5 10

gtc tta gat ggt tta aca cag caa gca gag ctc cag ctg ccc ctc ttc 100
Val Leu Asp Gly Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe
15 20 25

ctc ctg ttc ctg gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc 148
Leu Leu Phe Leu Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly
30 35 40

atg att ctc ctg att gca gtc agc cct cta ctt cac acc ccc atg tac 196

Met Ile Leu Leu Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr
45 50 55 60

tat ttc ctc agc agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc 244
Tyr Phe Leu Ser Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val
65 70 75

att act ccc aaa atg ctg gtg aac ttc cta gga aag aag aat aca atc 292
Ile Thr Pro Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile
80 85 90

ctt tac tct gag tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg 340
Leu Tyr Ser Glu Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val
95 100 105

gtg gct gag ggt tac ctc ctg act gcc atg gca tat gat cgc tat gtt 388
Val Ala Glu Gly Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val
110 115 120

gcc atc tgt agc cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc 436
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val
125 130 135 140

tgc tca ctg cta gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc 484
Cys Ser Leu Leu Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala
145 150 155

ttg act cat aca agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac 532
Leu Thr His Thr Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His
160 165 170

att atc aac cat tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc 580
Ile Ile Asn His Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser
175 180 185

tgc tcc aac aca cac ctc aat gag ctt cta ctt ttt atc att gcg ggg 628
Cys Ser Asn Thr His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly
190 195 200

ttt aac acc ttg gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc 676
Phe Asn Thr Leu Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe
205 210 215 220

atc ctc tac agc atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa 724
Ile Leu Tyr Ser Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys
225 230 235

gct ttt gga aca tgc agc tct cat ctc atg gct gtg gt 762
Ala Phe Gly Thr Cys Ser Ser His Leu Met Ala Val
240 245

<210> 33

<211> 248

<212> PRT

<213> Homo sapiens

<400> 33

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
1 5 10 15

Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20 25 30

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
35 40 45

Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50 55 60

Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
65 70 75 80

Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
85 90 95

Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
100 105 110

Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
115 120 125

Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
130 135 140

Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
145 150 155 160

Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
165 170 175

Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
180 185 190

His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
195 200 205

Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
210 215 220

Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225 230 235 240

Cys Ser Ser His Leu Met Ala Val

245

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthsized primer sequence

<400> 34

gaagagcagt gagggtccat gttaagg 27

<210> 35

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 35

cagcagcttg tccttcgtcg atttctgc 28

<210> 36

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 36

gctagggtgg gcaccaaggt gttaaaccc 29

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 37

tgcaaaagga cagtttcatc atggcac 27

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 38

caaagaactc acccaaattc ctacagct 28

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 39

catggtaggc aaccttggct tgatcac 27

<210> 40

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 40

gtttattaaa tcacacataa caccatctg 29

<210> 41

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 41

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<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 42

caaagaactc acccaaattc ctacagcc 28

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 43

catggtaggc aaccttggct tgatcat 27

<210> 44

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 44

gtttattaaa tcacacataa caccatctg 29

<210> 45

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 45

cagagacaga gcaatgacat gagagctac 29

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 46

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<210> 47

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 47

cctttataga tctctgttat tcctgtgtg 29

<210> 48

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 48

tcggttgcca gtgatatgaa gagaccc 27

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 49

ggctttggat ctgccctctg cagaagg 27

<210> 50

<211> 450

<212> DNA

<213> Homo sapiens

<400> 50

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gaacttccta ggaaagaaga atacaatcct ttactctgag tgcatggtcc agctcttttt 120

ctttgtggtc tttgtggtgg ctgagggtta cctcctgact gccatggcat atgatcgcta 180

tgttgccatc tgtagcccac tgctttataa tgcgatcatg tcctcatggg tctgctcact 240

gctagtgctg gctgccttct tcttgggctt tctctctgcc ttgactcata caagtgccat 300

gatgaaactg tccttttgca aatcccacat tatcaaccat tacttctgtg atgttcttcc 360

cctcctcaat ctctcctgct ccaacacaca cctcaatgag cttctacttt ttatcattgc 420

ggggtttaac accttggtgc ccaccctagc 450

<210> 51

<211> 637

<212> DNA

<213> Homo sapiens

<400> 51

catggtaggc aaccttggct tgatcactct tttcggtcta aattctcacc tccacacacc 60

aatgtactat ttcctcttca atctctcctt cattgatctc tgttactcct ctgttttcac 120

tcccaaaatg ctaatgaact ttgtgtcaaa aaagaatatt atctccaatg ttgggtgcat 180

gactcggctg tttttctttc tctttttcgt catctctgaa tgttacatgt tgacctcaat 240

ggcatatgat cgctatgtgg ccatctgtaa tccattgctg tataaggtca ccatgtccca 300

tcaggtctgt tctatgctca cttttgctgc ttacataatg ggattggctg gagccacggc 360

ccacaccggg tgcatgttta gactcacctt ctgcagtgct aatatcatta accattactt 420

gtgtgacata ctccccctcc tccagctttc ctgcaccagc acctatgtca acgaggtggt 480

tgttctcatt gttgtgggta ctaatatcac ggtacccagt tgtaccatcc tcatttctta 540

tgttttcatt gtcactagca ttcttcatat caaatccact caaggaagat caaaagcctt 600

cagtacttgt agctctcatg tcattgctct gtctctg 637

<210> 52

<211> 637

<212> DNA

<213> Homo sapiens

<400> 52

catggtaggc aaccttggct tgatcattct tttcggtcta aattctcacc tccacacacc 60

aatgtactat ttcctcttca atctctcctt cattgatctc tgttactcct ctgttttcac 120

tcccaaaatg ctaatgaact ttgtatcaaa aaagaatatt atctcctatg ttgggtgcat 180

gactcagctg tttttctttc tctttttttgt catctctgaa tgctacatat tgacctcaat 240

ggcatatgat cgctatgtgg ccatctgtaa tccattgctg tataaggtca ccatgtccca 300

tcaggtctgt tctatgctca cttttgctgc ttacataatg ggattggctg gagccacggc 360

ccacaccggg tgcatgctta gactcacctt ctgcagtgct aatatcatca accattactt 420

gtgtgacata ctccccctcc tccagctttc ctgcaccagc acctatgtca acgaggtggt 480

tgttctcatt gttgtgggta ttaatatcat ggtacccagt tgtaccatcc tcatttctta 540

tgttttcatt gtcactagca ttcttcatat caaatccact caaggaagat caaaagcctt 600

cagtacttgt agctctcatg tcattgctct gtctctg 637

<210> 53

<211> 509

<212> DNA

<213> Homo sapiens

<400> 53

cctttataga tctctgttat tcctgtgtgt ttacccccaa aatgctgaat gactttgttt 60

cagaaagtat catctcttat gtgggatgta tgactcagct atttttcttc tgtttctttg 120

tcaattctga gtgctatgtg ttggtatcaa tggcctatga tcgctatgtg gccatctgca 180

acccccctgct ctacatggtc accatgtccc caagggtctg ctttctgctg atgtttggtt 240

cctatgtggt agggtttgct ggggccatgg cccacactgg aagcatgctg cgactgacct 300

tctgtgattc caacgtcatt gaccattatc tgtgtgacgt tctccccctc ttgcagctct 360

cctgcaccag cacccatgtc agtgagctgg tatttttcat tgttgttgga gtaatcacca 420

tgctatccag cataagcatc gtcatctctt acgctttgat actctccaac atcctctgta 480

ttccttctgc agagggcaga tccaaagcc 509